

## SEQUENCE LISTING

<110> National Research Council of Canada

<120> Overexpression in Yeast and Plants of a Gene Encoding  
Glycerol 3-Phosphate Acyltransferase

<130> 44838-PT

<140>

<141>

<150> US 60/139788

<151> 1999-06-21

<150> US 60/182905

<151> 2000-02-16

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 1671

<212> DNA

<213> *Carthamus tinctorius*

<400> 1

tctctctctc tcacacacaa cacacaaaac acacactact gctactttct ctctctacta 60  
cactctctc tcgctatgct gatcttcttc tctccttctt ccctactct cttcttctcc 120  
accacaaacg caaatcctag ggtttctcct tcatcttcac cttcttctgc cttcactcct 180  
cctctgtctt cttctcgctt ccgcccgcatt ctccgggggt ttccgtgcct cgcgttctct 240  
gcgccggcga atgccgccca tggcacggcg gagaccgtcc acggcaacaa gtggccgtca 300  
ccgtcgtcct cctcctctgc tgctacgcaa ccgtccgctg gatccgacca cggtcactct 360  
cgtacattca tcgatgctcg ttccgaacaa gatcttcttt ctggaattca aagagagttg 420  
gaagctggaa cactgccaaa acatattgct caagcaatgg aggagctata tcagaactac 480  
aaaaatgcag ttctccaaag tgcggctcct catgcagaag atattgtgtt gtcaaacatg 540  
cgtgtagcgt ttgatcgtat gttcttggat gtgaaggagc cgtttgaatt ttcaccatat 600  
catgaagcta ttttggaacc ttttaactac tatatgtttg gtcaaaatta tatteggcct 660

```

ttggtcaatt tcagggaaatc atacgttggc aatgtotccg ttttcggtgt aatggaagag 720
cagcttaagc agggtgacaa cgtgggttttg atctcaaacc atcaaacaga agcagatcca 780
gctgttattg ccttgatgct tgaaacaaca aacccccata tttctgagaa cataatctac 840
gtggcagggg atagagtaat aacagatcct ctttgcaagc ctttcagcat ggggaaggaat 900
ctggttgctg tgtattcaaa aaagcatatg aatgatgttc ctgagcttgc tgagatgaaa 960
aaaagatcaa atacaagaag tttaaaagag atggctttgc ttttgagggg cggatctaaa 1020
ataatatgga ttgcgccaag tgggtggcagg gacaggccag atcctatcac aaatcagtgg 1080
tttccggcac cgtttgatgc cacttcgctt gacaacatga gaaggctcgt ggaccatgct 1140
ggtttggtgg gtcacatata tcctttagcc atattgtgcc atgacatcat gccccctcct 1200
cttcaggttg agaaagaaat tggagagaag aggttgatct cttttcatgg caccggaata 1260
tcagtggcac cggaaattaa tttccaagaa gttactgcct cttgtgggtc ccccgaggag 1320
gcgaaggcag cttattcaca ggcactctat gattccgtgt gtgaacaata caaggtgcta 1380
cattctgcgg tacatggagg aaaagggtta gaagcatcaa caccaagtgt ctcgttgtca 1440
caacccttgc agtttctcga ttagtctctt ggttttagagg aggtgaaagc atattctttt 1500
gttttagatga cataggtgta tagatgatac cgaagaatag atgtacaaac aagtgataga 1560
aagatgtatg tctaataaaa aaatgttttc tgcattctgt aaagggatct tcaaaacaga 1620
ccttttatatt tagctgcagc aaccaatata tcaaaacagg tttttctttt t 1671

```

&lt;210&gt; 2

&lt;211&gt; 1130

&lt;212&gt; DNA

<213> *Carthamus tinctorius*

&lt;400&gt; 2

```

ggatccatgc acggtcactc tcgtacattc atcgatgctc gttccgaaca agatcttctt 60
tctggaattc aaagagagtt ggaagctgga aactgccaa aacatattgc tcaagcaatg 120
gaggagctat atcagaacta caaaaatgca gttctccaaa gtgcggctcc tcatgcagaa 180
gatattgtgt tgtcaaacat gcgtgtagcg tttgatcgta tgttcttgga tgtgaaggag 240
ccgtttgaat tttcaccata tcatgaagct attttggaac cttttaacta ctatatgttt 300
gggtcaaaatt atattcggcc tttggtcaat ttcagggaat catacgttgg caatgtctcc 360
gttttcggtg taatggaaga gcagcttaag cagggtgaca aggtggtttt gatctcaaac 420
catcaaacag aagcagatcc agctgttatt gccttgatgc ttgaaacaac aaacccccat 480
atctctgaga acataatcta cgtggcaggg gatagagtaa taacagatcc tctttgcaag 540
cctttcagca tgggaaggaa tctgttgctg gtgtattcaa aaaagcatat gaatgatgtt 600
cctgagcttg ctgagatgaa aaaaagatca aatacaagaa gtttaaaaga gatggctttg 660
cttttgaggg gcggatctaa aataatatgg attgcgccaa gtggtggcag ggacaggcca 720
gatcctatca caaatcagtg gtttccggca ccgtttgatg ccacttcgct tgacaacatg 780
agaaggctcg tggaccatgc tggtttggtg ggtcacatat atcctttagc catattgtgc 840
catgacatca tgccccctcc tcttcagggt gagaaagaaa ttggagagaa gaggttgatc 900

```

tctttttcatg gcaccggaat atcagtggca ccggaaatta atttccaaga agttactgcc 960  
 tcttgtgggt cccccgagga ggcgaaggca gcttattcac aggcaactcta tgattccgtg 1020  
 tgtgaacaat acaaggtgct acattctgcg gtacatggag gaaaagggtt agaagcatca 1080  
 acaccaagtg tctcgttgct acaacccttg cagtttctcg attaggatcc 1130

<210> 3

<211> 1130

<212> DNA

<213> *Carthamus tinctorius*

<400> 3

ggatccatgc acggtcactc tcgtacattc atcgatgctc gttccgaaca agatcttctt 60  
 tctggaattc aaagagagtt ggaagctgga aactgccaa aacatattgc tcaagcaatg 120  
 gaggagctat atcagaacta caaaaatgca gttctccaaa gtgcggctcc tcatgcagaa 180  
 gatatttgtt tgtcaaacat gcgtgtagcg tttgatcgta tgttcttgga tgtgaaggag 240  
 ccgtttgaat tttcaccata tcatgaagct attttggaaac cttttaacta ctatatgttt 300  
 ggtcaaaaatt atattcggcc tttggtcaat ttcagggaat catacgttgg caatgtctcc 360  
 gttttcggtg taatggaaga gcagcttaag cagggtgaca aggtgggttt gatctcaaac 420  
 catcaaacag aagcagatcc agctgttatt gccttgatgc ttgaaacaac aaacccccat 480  
 atttctgaga acataatcta cgtggcaggg gatagagtaa taacagatcc tctttgcaag 540  
 cctttcagca tgggaaggaa tctgttgctc gtgtattcaa aaaagcatat gaatgatgtt 600  
 cctgagcttg ctgagatgaa aaaaagatca aatacaagaa gtttaaaaga gatggctttg 660  
 cttttgaggg gcggatctaa aataatatgg attgcgccaa gtggtggcag ggacaggcca 720  
 gatcctatca caaatcagtg gtttccggca ccgtttgatg ccacttcgct tgacaacatg 780  
 agaaggctcg tggaccatgc tggtttggtg ggtcacatat atcctttagc catattgtgc 840  
 catgacatca tgccccctcc tcttcaggtt gagaaagaaa ttggagagaa gaggttgatc 900  
 tctttttcatg gcaccggaat atcagtggca ccggaaatta atttccaaga agttactgcc 960  
 tcttgtgggt cccccgagga ggcgaaggca gcttattcac aggcaactcta tgattccgtg 1020  
 tgtgaacaat acaaggtgct acattctgcg gtacatggag gaaaagggtt agaagcatca 1080  
 acaccaagtg tctcgttgct acaaccaag cagaaactcg attaggatcc 1130

<210> 4

<211> 2502

<212> DNA

<213> *Escherichia coli*

<400> 4

agatcttccc atgactttct gctatccttg ccgcgcattt gcattattaa ccagaggctt 60  
 tacatcgttt atgtccggct ggccacgaat ttactacaaa ttactgaatt taccattaag 120

catcctggta aaaagcaagt ctattccggc agatcctgcc ccggaactgg ggctggatac 180  
ctctcgcca attatgtacg ttttaccgta caactcgaaa gcagatttgc tgacgttgcg 240  
cgcccagtggt ctggcacatg acttgccctga cccgttagag ccgctggaaa tcgacggcac 300  
gctactgccg cgctatgtgt tcattcacgg cgggcccggt gtgttcacct attacacgcc 360  
gaaagaagag tctattaagc tgttccacga ctatctcgat ttgcaccgta gcaacccaaa 420  
tctggatgtg cagatgggtgc cagtgtcggg gatgtttggg cgcgcgcggg ggcgtgaaaa 480  
aggcgaagtg aaccgcggcgc tgcgtatgct taacggcgta cagaaatttt tcgctgtact 540  
gtggctcggt cgcgacagtt ttgtgcgttt ctgcgcgtca gtttcgctgc gccgtatggc 600  
ggatgaacac ggcacggata aaactatcgc tcagaaactg gcgcgcgtgg cgcgtatgca 660  
ctttgcccgt caacgtctgg ctgccgtagg cccacgtttg cctgctcgtc aggatctggt 720  
taataagctg ctgcgcctccc gcgccattgc caaagcggta gaagatgaag cgcgcagcaa 780  
aaaaatctcc catgaaaaag cgcagcagaa cgcgattgca ctgatggaag agattgcggc 840  
gaatttctct tacgagatga ttgcctgac tgaccgtatt ctgggcttca cctggaaccg 900  
actttaccag ggcatacaacg tccataacgc tgagcgcgtt cgcagctgg cccacgacgg 960  
tcatgagctg gtatatgtgc cttgccaccg cagtcacatg gactacctgc tgctttctta 1020  
cgtgctgtat caccaggggc tgggtgccgc gcatacgc gccgggatca acctgaattt 1080  
ctggcctgcc gggcgatatt tccgccgtct gggggcggtt tttattcgcc gtacgtttaa 1140  
aggcaataaa ctttattcca ccgttttccg ggagtatctc ggcaactgt tcagccgtgg 1200  
ttattccgtc gagtacttcg tgggaaggcg tcgttcccgt acggggcggt tgctggatcc 1260  
gaaaactggg acgctgtcga tgaccattca ggcgatgctg cgtggcgcca cgcgtccgat 1320  
tacgtgatt ccgatctata tcggttatga gcacgtcatg gaagtgggta cttacgcca 1380  
agaactgcgc ggcgcgacga aagagaaaga gagcctgccg cagatgctgc gcggtttaag 1440  
caagctcgt aatctcggtc agggttacgt caacttcggt gaaccaatgc cgttgatgac 1500  
ctacctaac cagcatgtac ctgactggcg tgaatctatc gatcccatcg aagcgggtgcg 1560  
tccggcatgg ttaacgccga cggtaataa tattgctgcc gatctgatgg tacgcattaa 1620  
caacgcaggc gcggcaaacg ccatgaacct gtgctgtact gcgctactgg catcacgtca 1680  
gcgctcactc accgcgagc agttaaccga gcaactcaac tgctacctgg atctgatgcg 1740  
caacgtgcc tactccacgg actctaccgt tccttcagcc agcgcacgcg agcttatcga 1800  
tcacgcgctg caaatgaaca agtttgaagt cgagaaagac acaatcggcg acatcatcat 1860  
tctgccgcgc gagcaagcgg tgcgtgatgac ctactatcgc aacaacattg cgcataatgtt 1920  
gggtgctgcct tcgctgatgg cgacaatcgt caccagcat cgccacatct cccgcgacgt 1980  
attgatggag cacgtcaatg tgctttaccc aatgctgaaa gcggagctgt tcctgcgctg 2040  
ggatcgcgac gagttgccgg acgttattga tgcgctggca aatgagatgc aacgtcaggg 2100  
gctgattacc ctgcaagatg atgagttgca tatcaaccgc gcgcattctc gcacgctaca 2160  
gctgctggcc gcaggcgcgc gcgaaacgct gcaacggtat gccatcacct tctggttgtt 2220  
gagtgccaac ccgtcgatca accgcggtac gctggagaaa gagagccgca ccgtcgcgca 2280  
acgtctctcc gtgctgcacg gcatcaacgc gccggagttc ttcgacaagg cgggtgttcag 2340  
ttctctggtg ctgacactgc gtgatgaagg gtatatcagc gatagcggcg atgccgaacc 2400

ggcagaaacg atgaagggtt atcagttgct ggcggagttg attacatcag acgtgcgttt 2460  
gacgattgag agtgcgacgc agggcgaagg gtaatcagat ct 2502

<210> 5

<211> 2502

<212> DNA

<213> *Escherichia coli*

<400> 5

agatcttccc atgactttct gctatccttg ccgcgcattt gcattattaa ccagaggctt 60  
tacatcgttt atgtccggct ggccacgaat ttactacaaa ttactgaatt taccattaag 120  
catcctggta aaaagcaagt ctattccggc agatcctgcc ccggaactgg ggctggatac 180  
ctctcgtcca attatgtacg ttttaccgta caactcgaaa gcagatttgc tgacgttgcg 240  
cgcccagtgt ctggcacatg acttgctga cccgttagag ccgctggaaa tcgacggcac 300  
gctactgccg cgctatgtgt tcattcacgg cgggcccgcgt gtgttcacct attacacgcc 360  
gaaagaagag tctattaagc tgttcacga ctatctcgat ttgcaccgta gcaacccaaa 420  
tctggatgtg cagatgggtgc cagtgtcggg gatgtttggg cgcgcgccgg ggcgtgaaaa 480  
aggcgaagtg aaccgcgcgc tgcgtatgct taacggcgta cagaaatttt tcgctgtact 540  
gtggctcggg cgcgacagtt ttgtgcgttt ctgcgcgtca gtttcgctgc gccgtatggc 600  
ggatgaacac ggcacggata aaactatcgc tcagaaaactg gcgcgcgtgg cgcgtatgca 660  
ctttgcccgt caacgtctgg ctgccgtagg cccacgtttg cctgctcgtc aggatctggt 720  
taataagctg ctgcgcctccc gcgccattgc caaagcggta gaagatgaag cgcgcgagcaa 780  
aaaaatctcc catgaaaaag cgcagcagaa cgcgattgca ctgatggaag agattgcggc 840  
gaatttctct tacgagatga ttgcctgac tgaccgtatt ctgggcttca cctggaaccg 900  
actttaccag ggcattcaacg tccataacgc tgagcgcgtt cgccagctgg cccacgacgg 960  
tcatgagctg gtatatgtgc cttgccaccg cagtcacatg gactacctgc tgctttctta 1020  
cgtgctgtat caccaggggc tggcgccgcc gcataatcgc gccgggatca acctgaattt 1080  
ctggcctgcc gggccgattt tccgcgtctt gggggcgctt tttattcgcc gtacgtttaa 1140  
aggcaataaa ctttattcca ccgttttccg ggagtatctc ggcgaactgt tcagccgtgg 1200  
ttattccgtc gagtacttcg tggaaggcgg tcgttcccgt acggggcggt tgctggatcc 1260  
gaaaactggg acgctgtcga tgaccattca ggcgatgctg cgtggcggca cgcgtccgat 1320  
tacgctgatt ccgatctata tcggttatga gcacgtcatg gaagtgggta cttacgcaa 1380  
agaactgcgc ggcgcgacga aagagaaaga gagcctgccg cagatgctgc gcggtttaag 1440  
caagctgcgt aatctcggtc agggttacgt caacttcggg gaaccaatgc cgttgatgac 1500  
ctaccttaac cagcatgtac ctgactggcg tgaatctatc gatcccatcg aagcgggtgcg 1560  
tccggcatgg ttaacgccga cggtaataa tattgctgcc gatctgatgg tacgcattaa 1620  
caacgcaggc gcggcaaacg ccatgaacct gtgctgtact gcgctactgg catcacgtca 1680  
gcgctcactc acccgcgagc agttaaccga gcaactcaac tgctacctgg atctgatgcg 1740  
caacgtgccc tactccacgg actctaccgt tccttcagcc agcgccagcg agcttatcga 1800

6/21

tcacgcgctg caaatgaaca agtttgaagt cgagaaagac acaatcggcg acatcatcat 1860  
 tctgccgcgc gagcaagcgg tgctgatgac ctactatcgc aacaacattg cgcataatgtt 1920  
 ggtgctgcct tcgctgatgg cggcaatcgt caccagcat cgccacatct cccgcgacgt 1980  
 attgatggag cacgtcaatg tgctttaccc aatgctgaaa gcggagctgt tcttgcgctg 2040  
 ggatcgcgac gagttgccgg acgttattga tgcgctggca aatgagatgc aacgtcaggg 2100  
 gctgattacc ctgcaagatg atgagttgca tatcaaccgg gcgcattctc gcacgctaca 2160  
 gctgctggcc gcaggcgcgc gcgaaacgct gcaacgttat gccatcacct tctggttggt 2220  
 gagtgccaac ccgtcgatca accgcggtac gctggagaaa gagagccgca ccgtcgcgca 2280  
 acgtctctcc gtgctgcacg gcatcaacgc gccggagttc ttcgacaagg cgggtgttcag 2340  
 ttctctggtg ctgacactgc gtgatgaagg gtatatcagc gatagcggcg atgccgaacc 2400  
 ggcagaaacg atgaaggttt atcagttgct ggcggagttg attacatcag acgtgcggtt 2460  
 gacgattgag agtgcgaagc agaaggaagg gtaatcagat ct 2502

&lt;210&gt; 6

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Carthamus tinctorius

&lt;400&gt; 6

Ser Leu Ser Leu Thr His Asn Thr Gln Asn Thr His Tyr Cys Tyr Phe  
 1 5 10 15

Leu Ser Leu Leu His Ser Pro Leu Ala Met Ser Ile Phe Phe Ser Pro  
 20 25 30

Ser Ser Pro Thr Leu Phe Phe Ser Thr Thr Asn Ala Asn Pro Arg Val  
 35 40 45

Ser Pro Ser Ser Ser Pro Ser Ser Ala Phe Thr Pro Pro Leu Ser Ser  
 50 55 60

Ser Arg Leu Arg Pro Ile Leu Arg Gly Phe Pro Cys Leu Ala Phe Ser  
 65 70 75 80

Ala Pro Ala Asn Ala Ala His Gly Thr Ala Glu Thr Val His Gly Asn  
 85 90 95

Lys Trp Pro Ser Pro Ser Ser Ser Ser Ala Ala Thr Gln Pro Ser  
 100 105 110

WO 00/78974

PCT/CA00/00738

7/21

Ala Gly Ser Asp His Gly His Ser Arg Thr Phe Ile Asp Ala Arg Ser  
 115 120 125

Glu Gln Asp Leu Leu Ser Gly Ile Gln Arg Glu Leu Glu Ala Gly Thr  
 130 135 140

Leu Pro Lys His Ile Ala Gln Ala Met Glu Glu Leu Tyr Gln Asn Tyr  
 145 150 155 160

Lys Asn Ala Val Leu Gln Ser Ala Ala Pro His Ala Glu Asp Ile Val  
 165 170 175

Leu Ser Asn Met Arg Val Ala Phe Asp Arg Met Phe Leu Asp Val Lys  
 180 185 190

Glu Pro Phe Glu Phe Ser Pro Tyr His Glu Ala Ile Leu Glu Pro Phe  
 195 200 205

Asn Tyr Tyr Met Phe Gly Gln Asn Tyr Ile Arg Pro Leu Val Asn Phe  
 210 215 220

Arg Glu Ser Tyr Val Gly Asn Val Ser Val Phe Gly Val Met Glu Glu  
 225 230 235 240

Gln Leu Lys Gln Gly Asp Asn Val Val Leu Ile Ser Asn His Gln Thr  
 245 250 255

Glu Ala Asp Pro Ala Val Ile Ala Leu Met Leu Glu Thr Thr Asn Pro  
 260 265 270

His Ile Ser Glu Asn Ile Ile Tyr Val Ala Gly Asp Arg Val Ile Thr  
 275 280 285

Asp Pro Leu Cys Lys Pro Phe Ser Met Gly Arg Asn Leu Leu Cys Val  
 290 295 300

Tyr Ser Lys Lys His Met Asn Asp Val Pro Glu Leu Ala Glu Met Lys  
 305 310 315 320

WO 00/78974

PCT/CA00/00738

8/21

Lys Arg Ser Asn Thr Arg Ser Leu Lys Glu Met Ala Leu Leu Leu Arg  
 325 330 335

Gly Gly Ser Lys Ile Ile Trp Ile Ala Pro Ser Gly Gly Arg Asp Arg  
 340 345 350

Pro Asp Pro Ile Thr Asn Gln Trp Phe Pro Ala Pro Phe Asp Ala Thr  
 355 360 365

Ser Leu Asp Asn Met Arg Arg Leu Val Asp His Ala Gly Leu Val Gly  
 370 375 380

His Ile Tyr Pro Leu Ala Ile Leu Cys His Asp Ile Met Pro Pro Pro  
 385 390 395 400

Leu Gln Val Glu Lys Glu Ile Gly Glu Lys Arg Leu Ile Ser Phe His  
 405 410 415

Gly Thr Gly Ile Ser Val Ala Pro Glu Ile Asn Phe Gln Glu Val Thr  
 420 425 430

Ala Ser Cys Gly Ser Pro Glu Glu Ala Lys Ala Ala Tyr Ser Gln Ala  
 435 440 445

Leu Tyr Asp Ser Val Cys Glu Gln Tyr Lys Val Leu His Ser Ala Val  
 450 455 460

His Gly Gly Lys Gly Leu Glu Ala Ser Thr Pro Ser Val Ser Leu Ser  
 465 470 475 480

Gln Pro Leu Gln Phe Leu Asp  
 485

&lt;210&gt; 7

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Carthamus tinctorius



WO 00/78974

PCT/CA00/00738

9/21

&lt;400&gt; 7

Gly Ser Met His Gly His Ser Arg Thr Phe Ile Asp Ala Arg Ser Glu  
 1 5 10 15

Gln Asp Leu Leu Ser Gly Ile Gln Arg Glu Leu Glu Ala Gly Thr Leu  
 20 25 30

Pro Lys His Ile Ala Gln Ala Met Glu Glu Leu Tyr Gln Asn Tyr Lys  
 35 40 45

Asn Ala Val Leu Gln Ser Ala Ala Pro His Ala Glu Asp Ile Val Leu  
 50 55 60

Ser Asn Met Arg Val Ala Phe Asp Arg Met Phe Leu Asp Val Lys Glu  
 65 70 75 80

Pro Phe Glu Phe Ser Pro Tyr His Glu Ala Ile Leu Glu Pro Phe Asn  
 85 90 95

Tyr Tyr Met Phe Gly Gln Asn Tyr Ile Arg Pro Leu Val Asn Phe Arg  
 100 105 110

Glu Ser Tyr Val Gly Asn Val Ser Val Phe Gly Val Met Glu Glu Gln  
 115 120 125

Leu Lys Gln Gly Asp Lys Val Val Leu Ile Ser Asn His Gln Thr Glu  
 130 135 140

Ala Asp Pro Ala Val Ile Ala Leu Met Leu Glu Thr Thr Asn Pro His  
 145 150 155 160

Ile Ser Glu Asn Ile Ile Tyr Val Ala Gly Asp Arg Val Ile Thr Asp  
 165 170 175

Pro Leu Cys Lys Pro Phe Ser Met Gly Arg Asn Leu Leu Cys Val Tyr  
 180 185 190

Ser Lys Lys His Met Asn Asp Val Pro Glu Leu Ala Glu Met Lys Lys  
 195 200 205

WO 00/78974

PCT/CA00/00738

10/21

Arg Ser Asn Thr Arg Ser Leu Lys Glu Met Ala Leu Leu Leu Arg Gly  
 210 215 220

Gly Ser Lys Ile Ile Trp Ile Ala Pro Ser Gly Gly Arg Asp Arg Pro  
 225 230 235 240

Asp Pro Ile Thr Asn Gln Trp Phe Pro Ala Pro Phe Asp Ala Thr Ser  
 245 250 255

Leu Asp Asn Met Arg Arg Leu Val Asp His Ala Gly Leu Val Gly His  
 260 265 270

Ile Tyr Pro Leu Ala Ile Leu Cys His Asp Ile Met Pro Pro Pro Leu  
 275 280 285

Gln Val Glu Lys Glu Ile Gly Glu Lys Arg Leu Ile Ser Phe His Gly  
 290 295 300

Thr Gly Ile Ser Val Ala Pro Glu Ile Asn Phe Gln Glu Val Thr Ala  
 305 310 315 320

Ser Cys Gly Ser Pro Glu Glu Ala Lys Ala Ala Tyr Ser Gln Ala Leu  
 325 330 335

Tyr Asp Ser Val Cys Glu Gln Tyr Lys Val Leu His Ser Ala Val His  
 340 345 350

Gly Gly Lys Gly Leu Glu Ala Ser Thr Pro Ser Val Ser Leu Ser Gln  
 355 360 365

Pro Leu Gln Phe Leu Asp  
 370

&lt;210&gt; 8

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Carthamus tinctorius

WO 00/78974

PCT/CA00/00738

11/21

&lt;400&gt; 8

Gly Ser Met His Gly His Ser Arg Thr Phe Ile Asp Ala Arg Ser Glu  
 1 5 10 15

Gln Asp Leu Leu Ser Gly Ile Gln Arg Glu Leu Glu Ala Gly Thr Leu  
 20 25 30

Pro Lys His Ile Ala Gln Ala Met Glu Glu Leu Tyr Gln Asn Tyr Lys  
 35 40 45

Asn Ala Val Leu Gln Ser Ala Ala Pro His Ala Glu Asp Ile Val Leu  
 50 55 60

Ser Asn Met Arg Val Ala Phe Asp Arg Met Phe Leu Asp Val Lys Glu  
 65 70 75 80

Pro Phe Glu Phe Ser Pro Tyr His Glu Ala Ile Leu Glu Pro Phe Asn  
 85 90 95

Tyr Tyr Met Phe Gly Gln Asn Tyr Ile Arg Pro Leu Val Asn Phe Arg  
 100 105 110

Glu Ser Tyr Val Gly Asn Val Ser Val Phe Gly Val Met Glu Glu Gln  
 115 120 125

Leu Lys Gln Gly Asp Lys Val Val Leu Ile Ser Asn His Gln Thr Glu  
 130 135 140

Ala Asp Pro Ala Val Ile Ala Leu Met Leu Glu Thr Thr Asn Pro His  
 145 150 155 160

Ile Ser Glu Asn Ile Ile Tyr Val Ala Gly Asp Arg Val Ile Thr Asp  
 165 170 175

Pro Leu Cys Lys Pro Phe Ser Met Gly Arg Asn Leu Leu Cys Val Tyr  
 180 185 190

Ser Lys Lys His Met Asn Asp Val Pro Glu Leu Ala Glu Met Lys Lys  
 195 200 205

WO 00/78974

PCT/CA00/00738

12/21

Arg Ser Asn Thr Arg Ser Leu Lys Glu Met Ala Leu Leu Leu Arg Gly  
 210 215 220

Gly Ser Lys Ile Ile Trp Ile Ala Pro Ser Gly Gly Arg Asp Arg Pro  
 225 230 235 240

Asp Pro Ile Thr Asn Gln Trp Phe Pro Ala Pro Phe Asp Ala Thr Ser  
 245 250 255

Leu Asp Asn Met Arg Arg Leu Val Asp His Ala Gly Leu Val Gly His  
 260 265 270

Ile Tyr Pro Leu Ala Ile Leu Cys His Asp Ile Met Pro Pro Pro Leu  
 275 280 285

Gln Val Glu Lys Glu Ile Gly Glu Lys Arg Leu Ile Ser Phe His Gly  
 290 295 300

Thr Gly Ile Ser Val Ala Pro Glu Ile Asn Phe Gln Glu Val Thr Ala  
 305 310 315 320

Ser Cys Gly Ser Pro Glu Glu Ala Lys Ala Ala Tyr Ser Gln Ala Leu  
 325 330 335

Tyr Asp Ser Val Cys Glu Gln Tyr Lys Val Leu His Ser Ala Val His  
 340 345 350

Gly Gly Lys Gly Leu Glu Ala Ser Thr Pro Ser Val Ser Leu Ser Gln  
 355 360 365

Pro Lys Gln Lys Leu Asp  
 370

&lt;210&gt; 9

&lt;211&gt; 827

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

WO 00/78974

PCT/CA00/00738

13/21

&lt;400&gt; 9

Met Thr Phe Cys Tyr Pro Cys Arg Ala Phe Ala Leu Leu Thr Arg Gly  
 1 5 10 15

Phe Thr Ser Phe Met Ser Gly Trp Pro Arg Ile Tyr Tyr Lys Leu Leu  
 20 25 30

Asn Leu Pro Leu Ser Ile Leu Val Lys Ser Lys Ser Ile Pro Ala Asp  
 35 40 45

Pro Ala Pro Glu Leu Gly Leu Asp Thr Ser Arg Pro Ile Met Tyr Val  
 50 55 60

Leu Pro Tyr Asn Ser Lys Ala Asp Leu Leu Thr Leu Arg Ala Gln Cys  
 65 70 75 80

Leu Ala His Asp Leu Pro Asp Pro Leu Glu Pro Leu Glu Ile Asp Gly  
 85 90 95

Thr Leu Leu Pro Arg Tyr Val Phe Ile His Gly Gly Pro Arg Val Phe  
 100 105 110

Thr Tyr Tyr Thr Pro Lys Glu Glu Ser Ile Lys Leu Phe His Asp Tyr  
 115 120 125

Leu Asp Leu His Arg Ser Asn Pro Asn Leu Asp Val Gln Met Val Pro  
 130 135 140

Val Ser Val Met Phe Gly Arg Ala Pro Gly Arg Glu Lys Gly Glu Val  
 145 150 155 160

Asn Pro Pro Leu Arg Met Leu Asn Gly Val Gln Lys Phe Phe Ala Val  
 165 170 175

Leu Trp Leu Gly Arg Asp Ser Phe Val Arg Phe Ser Pro Ser Val Ser  
 180 185 190

Leu Arg Arg Met Ala Asp Glu His Gly Thr Asp Lys Thr Ile Ala Gln  
 195 200 205

WO 00/78974

PCT/CA00/00738

14/21

Lys Leu Ala Arg Val Ala Arg Met His Phe Ala Arg Gln Arg Leu Ala  
 210 215 220

Ala Val Gly Pro Arg Leu Pro Ala Arg Gln Asp Leu Phe Asn Lys Leu  
 225 230 235 240

Leu Ala Ser Arg Ala Ile Ala Lys Ala Val Glu Asp Glu Ala Arg Ser  
 245 250 255

Lys Lys Ile Ser His Glu Lys Ala Gln Gln Asn Ala Ile Ala Leu Met  
 260 265 270

Glu Glu Ile Ala Ala Asn Phe Ser Tyr Glu Met Ile Arg Leu Thr Asp  
 275 280 285

Arg Ile Leu Gly Phe Thr Trp Asn Arg Leu Tyr Gln Gly Ile Asn Val  
 290 295 300

His Asn Ala Glu Arg Val Arg Gln Leu Ala His Asp Gly His Glu Leu  
 305 310 315 320

Val Tyr Val Pro Cys His Arg Ser His Met Asp Tyr Leu Leu Leu Ser  
 325 330 335

Tyr Val Leu Tyr His Gln Gly Leu Val Pro Pro His Ile Ala Ala Gly  
 340 345 350

Ile Asn Leu Asn Phe Trp Pro Ala Gly Pro Ile Phe Arg Arg Leu Gly  
 355 360 365

Ala Phe Phe Ile Arg Arg Thr Phe Lys Gly Asn Lys Leu Tyr Ser Thr  
 370 375 380

Val Phe Arg Glu Tyr Leu Gly Glu Leu Phe Ser Arg Gly Tyr Ser Val  
 385 390 395 400

Glu Tyr Phe Val Glu Gly Gly Arg Ser Arg Thr Gly Arg Leu Leu Asp  
 405 410 415

WO 00/78974

PCT/CA00/00738

15/21

Pro Lys Thr Gly Thr Leu Ser Met Thr Ile Gln Ala Met Leu Arg Gly  
 420 425 430

Gly Thr Arg Pro Ile Thr Leu Ile Pro Ile Tyr Ile Gly Tyr Glu His  
 435 440 445

Val Met Glu Val Gly Thr Tyr Ala Lys Glu Leu Arg Gly Ala Thr Lys  
 450 455 460

Glu Lys Glu Ser Leu Pro Gln Met Leu Arg Gly Leu Ser Lys Leu Arg  
 465 470 475 480

Asn Leu Gly Gln Gly Tyr Val Asn Phe Gly Glu Pro Met Pro Leu Met  
 485 490 495

Thr Tyr Leu Asn Gln His Val Pro Asp Trp Arg Glu Ser Ile Asp Pro  
 500 505 510

Ile Glu Ala Val Arg Pro Ala Trp Leu Thr Pro Thr Val Asn Asn Ile  
 515 520 525

Ala Ala Asp Leu Met Val Arg Ile Asn Asn Ala Gly Ala Ala Asn Ala  
 530 535 540

Met Asn Leu Cys Cys Thr Ala Leu Leu Ala Ser Arg Gln Arg Ser Leu  
 545 550 555 560

Thr Arg Glu Gln Leu Thr Glu Gln Leu Asn Cys Tyr Leu Asp Leu Met  
 565 570 575

Arg Asn Val Pro Tyr Ser Thr Asp Ser Thr Val Pro Ser Ala Ser Ala  
 580 585 590

Ser Glu Leu Ile Asp His Ala Leu Gln Met Asn Lys Phe Glu Val Glu  
 595 600 605

Lys Asp Thr Ile Gly Asp Ile Ile Ile Leu Pro Arg Glu Gln Ala Val  
 610 615 620

WO 00/78974

PCT/CA00/00738

16/21

Leu Met Thr Tyr Tyr Arg Asn Asn Ile Ala His Met Leu Val Leu Pro  
 625 630 635 640

Ser Leu Met Ala Thr Ile Val Thr Gln His Arg His Ile Ser Arg Asp  
 645 650 655

Val Leu Met Glu His Val Asn Val Leu Tyr Pro Met Leu Lys Ala Glu  
 660 665 670

Leu Phe Leu Arg Trp Asp Arg Asp Glu Leu Pro Asp Val Ile Asp Ala  
 675 680 685

Leu Ala Asn Glu Met Gln Arg Gln Gly Leu Ile Thr Leu Gln Asp Asp  
 690 695 700

Glu Leu His Ile Asn Pro Ala His Ser Arg Thr Leu Gln Leu Leu Ala  
 705 710 715 720

Ala Gly Ala Arg Glu Thr Leu Gln Arg Tyr Ala Ile Thr Phe Trp Leu  
 725 730 735

Leu Ser Ala Asn Pro Ser Ile Asn Arg Gly Thr Leu Glu Lys Glu Ser  
 740 745 750

Arg Thr Val Ala Gln Arg Leu Ser Val Leu His Gly Ile Asn Ala Pro  
 755 760 765

Glu Phe Phe Asp Lys Ala Val Phe Ser Ser Leu Val Leu Thr Leu Arg  
 770 775 780

Asp Glu Gly Tyr Ile Ser Asp Ser Gly Asp Ala Glu Pro Ala Glu Thr  
 785 790 795 800

Met Lys Val Tyr Gln Leu Leu Ala Glu Leu Ile Thr Ser Asp Val Arg  
 805 810 815

Leu Thr Ile Glu Ser Ala Thr Gln Gly Glu Gly  
 820 825



WO 00/78974

PCT/CA00/00738

17/21

&lt;210&gt; 10

&lt;211&gt; 827

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 10

Met Thr Phe Cys Tyr Pro Cys Arg Ala Phe Ala Leu Leu Thr Arg Gly  
 1 5 10 15

Phe Thr Ser Phe Met Ser Gly Trp Pro Arg Ile Tyr Tyr Lys Leu Leu  
 20 25 30

Asn Leu Pro Leu Ser Ile Leu Val Lys Ser Lys Ser Ile Pro Ala Asp  
 35 40 45

Pro Ala Pro Glu Leu Gly Leu Asp Thr Ser Arg Pro Ile Met Tyr Val  
 50 55 60

Leu Pro Tyr Asn Ser Lys Ala Asp Leu Leu Thr Leu Arg Ala Gln Cys  
 65 70 75 80

Leu Ala His Asp Leu Pro Asp Pro Leu Glu Pro Leu Glu Ile Asp Gly  
 85 90 95

Thr Leu Leu Pro Arg Tyr Val Phe Ile His Gly Gly Pro Arg Val Phe  
 100 105 110

Thr Tyr Tyr Thr Pro Lys Glu Glu Ser Ile Lys Leu Phe His Asp Tyr  
 115 120 125

Leu Asp Leu His Arg Ser Asn Pro Asn Leu Asp Val Gln Met Val Pro  
 130 135 140

Val Ser Val Met Phe Gly Arg Ala Pro Gly Arg Glu Lys Gly Glu Val  
 145 150 155 160

Asn Pro Pro Leu Arg Met Leu Asn Gly Val Gln Lys Phe Phe Ala Val  
 165 170 175

WO 00/78974

PCT/CA00/00738

18/21

Leu Trp Leu Gly Arg Asp Ser Phe Val Arg Phe Ser Pro Ser Val Ser  
 180 185 190

Leu Arg Arg Met Ala Asp Glu His Gly Thr Asp Lys Thr Ile Ala Gln  
 195 200 205

Lys Leu Ala Arg Val Ala Arg Met His Phe Ala Arg Gln Arg Leu Ala  
 210 215 220

Ala Val Gly Pro Arg Leu Pro Ala Arg Gln Asp Leu Phe Asn Lys Leu  
 225 230 235 240

Leu Ala Ser Arg Ala Ile Ala Lys Ala Val Glu Asp Glu Ala Arg Ser  
 245 250 255

Lys Lys Ile Ser His Glu Lys Ala Gln Gln Asn Ala Ile Ala Leu Met  
 260 265 270

Glu Glu Ile Ala Ala Asn Phe Ser Tyr Glu Met Ile Arg Leu Thr Asp  
 275 280 285

Arg Ile Leu Gly Phe Thr Trp Asn Arg Leu Tyr Gln Gly Ile Asn Val  
 290 295 300

His Asn Ala Glu Arg Val Arg Gln Leu Ala His Asp Gly His Glu Leu  
 305 310 315 320

Val Tyr Val Pro Cys His Arg Ser His Met Asp Tyr Leu Leu Leu Ser  
 325 330 335

Tyr Val Leu Tyr His Gln Gly Leu Val Pro Pro His Ile Ala Ala Gly  
 340 345 350

Ile Asn Leu Asn Phe Trp Pro Ala Gly Pro Ile Phe Arg Arg Leu Gly  
 355 360 365

Ala Phe Phe Ile Arg Arg Thr Phe Lys Gly Asn Lys Leu Tyr Ser Thr  
 370 375 380

WO 00/78974

PCT/CA00/00738

19/21

Val Phe Arg Glu Tyr Leu Gly Glu Leu Phe Ser Arg Gly Tyr Ser Val  
385 390 395 400

Glu Tyr Phe Val Glu Gly Gly Arg Ser Arg Thr Gly Arg Leu Leu Asp  
405 410 415

Pro Lys Thr Gly Thr Leu Ser Met Thr Ile Gln Ala Met Leu Arg Gly  
420 425 430

Gly Thr Arg Pro Ile Thr Leu Ile Pro Ile Tyr Ile Gly Tyr Glu His  
435 440 445

Val Met Glu Val Gly Thr Tyr Ala Lys Glu Leu Arg Gly Ala Thr Lys  
450 455 460

Glu Lys Glu Ser Leu Pro Gln Met Leu Arg Gly Leu Ser Lys Leu Arg  
465 470 475 480

Asn Leu Gly Gln Gly Tyr Val Asn Phe Gly Glu Pro Met Pro Leu Met  
485 490 495

Thr Tyr Leu Asn Gln His Val Pro Asp Trp Arg Glu Ser Ile Asp Pro  
500 505 510

Ile Glu Ala Val Arg Pro Ala Trp Leu Thr Pro Thr Val Asn Asn Ile  
515 520 525

Ala Ala Asp Leu Met Val Arg Ile Asn Asn Ala Gly Ala Ala Asn Ala  
530 535 540

Met Asn Leu Cys Cys Thr Ala Leu Leu Ala Ser Arg Gln Arg Ser Leu  
545 550 555 560

Thr Arg Glu Gln Leu Thr Glu Gln Leu Asn Cys Tyr Leu Asp Leu Met  
565 570 575

Arg Asn Val Pro Tyr Ser Thr Asp Ser Thr Val Pro Ser Ala Ser Ala  
580 585 590

WO 00/78974

PCT/CA00/00738

20/21

Ser Glu Leu Ile Asp His Ala Leu Gln Met Asn Lys Phe Glu Val Glu  
 595 600 605

Lys Asp Thr Ile Gly Asp Ile Ile Ile Leu Pro Arg Glu Gln Ala Val  
 610 615 620

Leu Met Thr Tyr Tyr Arg Asn Asn Ile Ala His Met Leu Val Leu Pro  
 625 630 635 640

Ser Leu Met Ala Ala Ile Val Thr Gln His Arg His Ile Ser Arg Asp  
 645 650 655

Val Leu Met Glu His Val Asn Val Leu Tyr Pro Met Leu Lys Ala Glu  
 660 665 670

Leu Phe Leu Arg Trp Asp Arg Asp Glu Leu Pro Asp Val Ile Asp Ala  
 675 680 685

Leu Ala Asn Glu Met Gln Arg Gln Gly Leu Ile Thr Leu Gln Asp Asp  
 690 695 700

Glu Leu His Ile Asn Pro Ala His Ser Arg Thr Leu Gln Leu Leu Ala  
 705 710 715 720

Ala Gly Ala Arg Glu Thr Leu Gln Arg Tyr Ala Ile Thr Phe Trp Leu  
 725 730 735

Leu Ser Ala Asn Pro Ser Ile Asn Arg Gly Thr Leu Glu Lys Glu Ser  
 740 745 750

Arg Thr Val Ala Gln Arg Leu Ser Val Leu His Gly Ile Asn Ala Pro  
 755 760 765

Glu Phe Phe Asp Lys Ala Val Phe Ser Ser Leu Val Leu Thr Leu Arg  
 770 775 780

Asp Glu Gly Tyr Ile Ser Asp Ser Gly Asp Ala Glu Pro Ala Glu Thr  
 785 790 795 800

WO 00/78974

PCT/CA00/00738

21/21

Met Lys Val Tyr Gln Leu Leu Ala Glu Leu Ile Thr Ser Asp Val Arg  
805 810 815

Leu Thr Ile Glu Ser Ala Lys Gln Lys Glu Gly  
820 825